

Figure 1

50
100
70 90 110
130 150 170
CCTACCGCCATGGAACAAACGGGACAGAACGCCGGCGCTTCGGGGCCCGGAAAAGG
M E O R G O N A P A A S G A R K R
190 210 230
CACGGCCCAGGACCCAGGGAGGGCGGGGAGGCAGGGCTGGGCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
250 270 290
CTTGTGCTCGTTGTCGCCGGTCTGCTGTTGGTCTCAGCTGAGTCTGCTTGATCACC
L V L V V A A V L L L V S A E S A L I T
310 330 350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGGCCCCACAACAAAAGAGGTCCAGCCCCCTCA
Q Q D L A P Q Q R A A P Q Q K R S S P S
370 390 410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAACGGTAGAGATTGCATCTCCTGC
E G L C P P G H H I S E D G R D C I S C
430 450 470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTCTGCTTGCCTGCACC
K Y G Q D Y S T H W N D L L F C L R C T
490 510 530
AGGTGTGATTCAAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAACACAGTGTGT
R C D S G E V E L S P C T T T R N T V C
550 570 590
CAGTGCAGAAGGACACCTTCCGGAAAGAAGATTCTCCTGAGATGTGCCCGAAGTGCCTGC
Q C E E G T F R E E D S P E M C R K C R
610 630 650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTGGTATTGTACACCCCTGGAGTGACATCGAA
T G C P R G M V K V G D C T P W S D I E
670 690 710
TGTGTCCACAAAGAACATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTGATT
C V H K E S G I I I G V T V A A V V L I
730 750 770
GTGGCTGTGTTGCAAGTCTTACTGTGGAAGAAAGTCCTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
790 810 830
ATCTGCTCAGGTGGTGGGGACCTGAGCGTGTGGACAGAACGCTCACAAACGACCTGGG
I C S G G G D P E R V D R S S Q R P G
850 870 890
GCTGAGGACAATGTCCTCAATGAGATCGTGGTATCTGCAGCCCACCCAGGTCCCTGAG
A E D N V L N E I V S I L Q P T Q V P E
910 930 950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q E M E V Q E P A E P T G V N M L S P G
970 990 1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAACGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E S E H L L E P A E A E R S Q R R R L L
1030 1050 1070

Figure 1 (continued)

GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTGCA
V P A N E G D P T E T L R Q C F D D F A
1090 1110 1130
GACTTGGTGCCTTGTACTCCTGGAGCCGCTCATGAGGAAGTTGGCCTCATGGACAAT
D L V P F D S W E P L M R K L G L M D N
1150 1170 1190
GAGATAAAAGGTGGCTAAAGCTGAGGCAGCGGCCACAGGGACACCTGTACACGATGCTG
E I K V A K A E A A G H R D T L Y T M L
1210 1230 1250
ATAAAGTGGTCAACAAAACCGGGCGAGATGCCCTGTCCACACCTGCTGGATGCCTTG
I K W V N K T G R D A S V H T L L D A L
1270 1290 1310
GAGACGCTGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E T L G E R L A K Q K I E D H L L S S G
1330 1350 1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCTAACGTGTGATTCTCTTC
K F M Y L E G N A D S A M S *
1390 1410 1430
GGAAGTGAGACCTCCCTGGTTACCTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
1450 1470 1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA
1510 1530 1550
TCACCCAGTGGATGGAACATCCTGTAACCTTCACTGCACTGGCATTATTTTATAAGC
1570 1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA

Figure 2

1	M - L G -	- - - - - I W T L L P L V L	h Fas protein
1	H G L S -	- - - - - T V P D L L L P L	h TNFR I Protein
1	H E Q R -	- - - - - P R G C A A V A A	DR3 protein
1	H E Q R G Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T	L V L	HLYBX88XXprotein
13	P S V A R R E S S K S V V N A Q V T D I N S K G L E L R K T V T V E T Q N L E G D	h Fas protein	
14	V L L E L V G I Y P S G V I G L V P H E G D R E K R D S V C P Q G K Y I H -	- h TNFR I Protein	
14	A E L E V L L G A R A Q G -	- - - - - G T R S P R - C D C A - G D F - H - DR3 protein	
41	V V A A V E L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G E	HLYBX88XXprotein	
53	H E D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T	h Fas protein	
52	P Q N N S I C C T K C H K G T Y L Y N D C P G P Q D T D C R E C E S G S F T A	h TNFR I Protein	
41	R K I G L E F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A	DR3 protein	
81	- - - - - C P P G H I S E D - - - - - G R D C I S C K Y G Q D Y S	HLYBX88XXprotein	
93	D K A H F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N	h Fas protein	
92	S E N H L 2 - H C L S C S K C R K Z M G Q V E I S C T V D R D T V C G C R K N	h TNFR I Protein	
81	W E N H H W S E C A R C Q A C D E Q A S O V A L E N C S A V A D T R C G C K P G	DR3 protein	
105	T E W N D L L F C L R C T R C D - - S G E V E L S P C T T T R N T V C Q C E E G	HLYBX88XXprotein	
133	F E - - - - - C N S T V - - - C E H C D P C T K - - - - - - - - - - - - - - - - -	h Fas protein	
131	Q Y R E Y W S E N L F Q C - - - F N C S L C L N - G T V H - - - - - L S C Q E	h TNFR I Protein	
121	W E V E C - - - Q V S O C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R	DR3 protein	
143	T E R E - - - - - E D S P E M C R K C -	HLYBX88XXprotein	
149	- - - - - C E H G I I - - - K E C - - - - - T L T S N T K C K E - - - - -	h Fas protein	
161	K Q N T W C T C H A G F F L R E N E C V S C S N C K K S L E C T F L C L P Q I E	h TNFR I Protein	
158	R D T B C G T C L P G F Y Z H G D G C V S C P T S T L G - S C P E R C A A V C G	DR3 protein	
163	G M V K V G D C T P - - - W S D I E C V - - - - - - - - - - - - - - - - - - -	HLYBX88XXprotein	
168	- - - - - E G S R S N L G W - - - - - E C L L - L L P I P L I V - - - - - W	h Fas protein	
201	N V K G T E D S G T V U L L P L V I F F G L C L S L L F I G L M Y R Y Q R - W	h TNFR I Protein	
197	M F W V Q V U L L A G L V V P L L L G A T L T Y T Y R H C W	DR3 protein	
189	W R Q - - - - - V T V A A V V L I V A V F - - V C K S L L W K K V L P Y L K G I C S	HLYBX88XXprotein	
190	V E R R E V Q K E T C R R H E K E N Q G S H E S - - - - - - - - - - - - - - -	h Fas protein	
240	- H S A L Y S I V V G G K S T P E K Z G E L E G T T T K P L A P N P S F S P T P G	h TNFR I Protein	
229	- P H R P L - V T A D E A G M B A L T P P P A T H L S P L D S A H T L L A P P D	DR3 protein	
221	- - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q P T Q	HLYBX88XXprotein	
213	- -	h Fas protein	
279	F T P T L G F S P V P S S T F T S S S T Y T P G D - C E N F A A P R R E V A P P	h TNFR I Protein	
257	S S E B K I C T V Q L V G N S W T P G Y P E T Q E A L C P Q V T W S W D Q L - - P	DR3 protein	
255	V P B Q E M E V O P A E - - - - - P T G V N M L S P G - - - E S E H L - - -	HLYBX88XXprotein	
213	- - - - - P T L N P E T V A I N L - - - S D V D L S K Y I T T I A G V M	h Fas protein	
313	Y Q G A D B I L A C A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A	h TNFR I Protein	
305	S R A I G G P A A A P T L S P - - - - - E S P A G S P A M M L Q P G E Q	DR3 protein	
283	- - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q	HLYBX88XXprotein	
241	T L S Q V - - - - - R G F V R R N G V N E A K I D E I K N D N V Q D T A	h Fas protein	
358	T L Y A V V E N V P P L R W K E F V R R L G L S D H E I D R L E L Q N G R C L R	h TNFR I Protein	
335	- L Y D V M D A V P A R R W K E F V R C L G L R E A B I E A V E V E I G R - F R	DR3 protein	
312	C F D D F A D L V P F D S M E P L M R K L G L M D N E I - K V A K A E A A G H R	HLYBX88XXprotein	
272	E O K V Q L L R N W H O L H G K K E A - Y D T L I K D E K K A N L C T L A E K I	h Fas protein	
395	E A Q V S M L A T E R R R T P H R E A T L E L L G R V L R D M D L L G C L E D I	h TNFR I Protein	
373	D O O Y E E M L K R W R O Q Q P - - - A G L G A V Y A A L E R M G L D G C V E D L	DR3 protein	
351	B T L Y T M L I K H V N K T G P - D A S V H T E L D A L E T L G E R L A K Q K I	HLYBX88XXprotein	
311	Q T I E E K D I T S D S E N S N F R N E I Q S L V	h Fas protein	
433	E E A E - - - - - C G P A A L P P A P S L R	h TNFR I Protein	
410	- - - - - R S R L Q R G E	DR3 protein	
390	E D H L L S S G K F M Y L E G N - - A C S A M S	HLYBX88XXprotein	

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

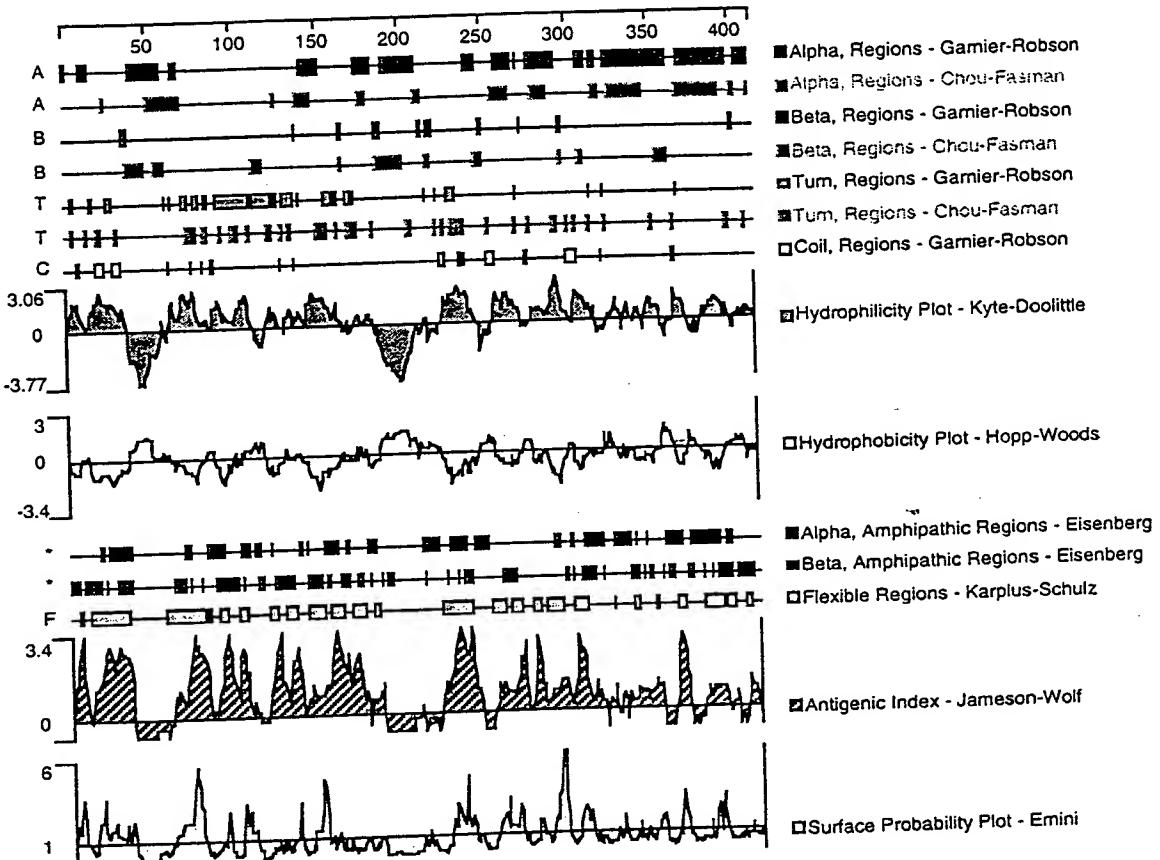


Figure 4

HAPBU13R

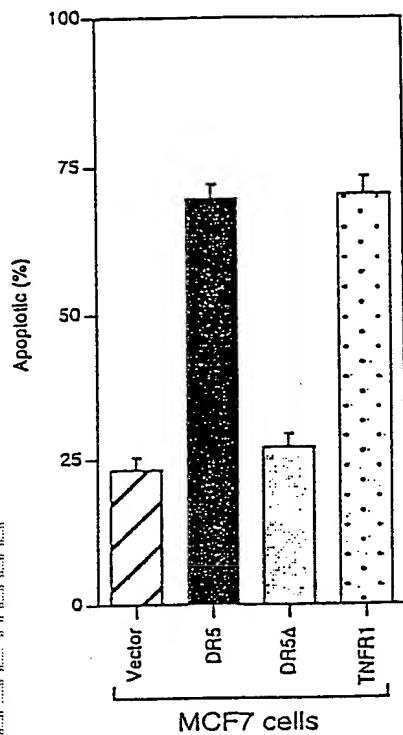
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51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTN ATCCCTAATG TNAAATGCNT NATTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNNTGG

HSBU76R

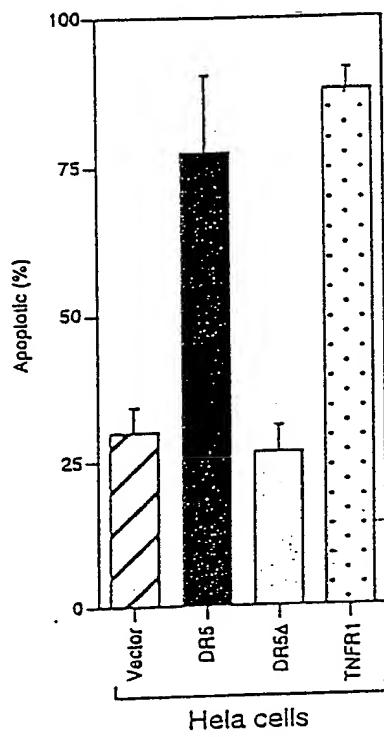
1 TTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
51 ATTTACATTA GGATAAAAAAA GTGCTGTGAA AACAAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT

Figure 5

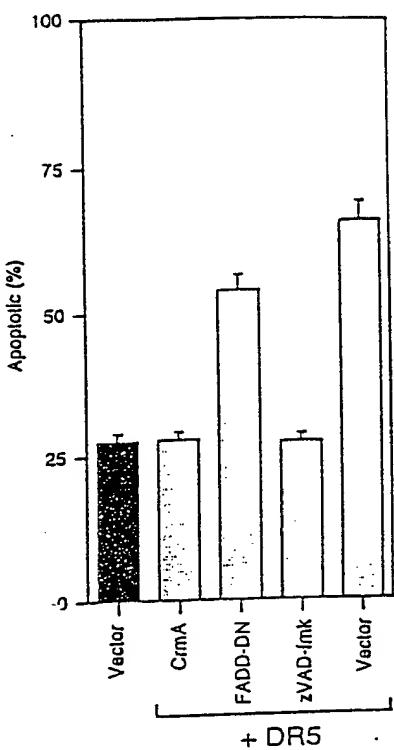
A



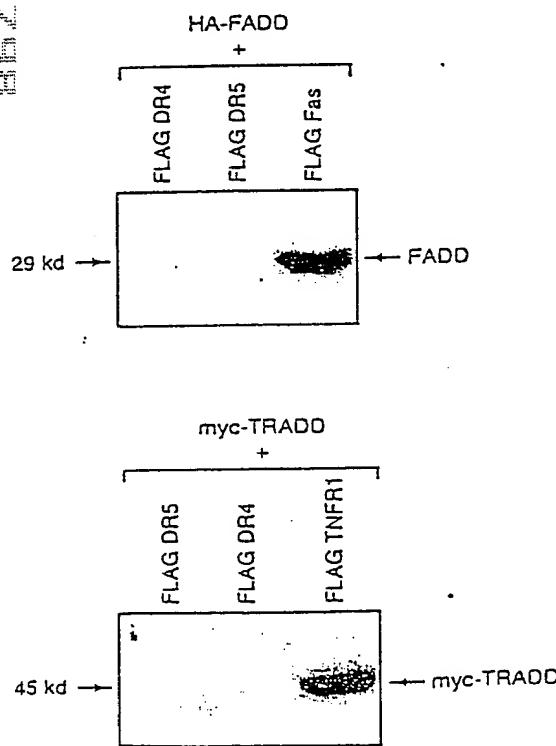
B



C



D



E

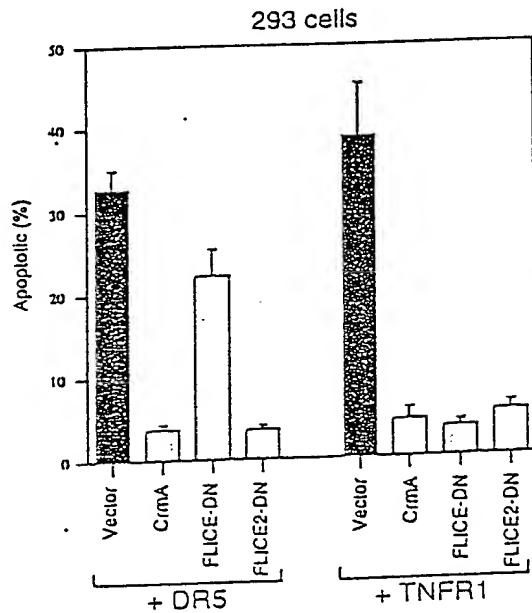
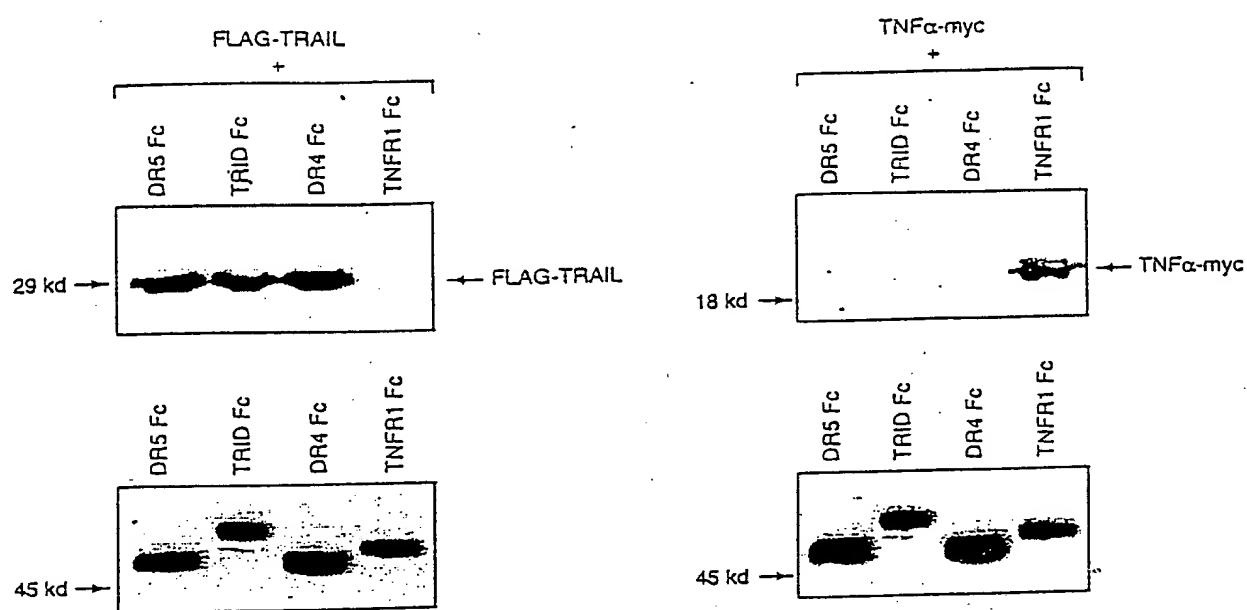
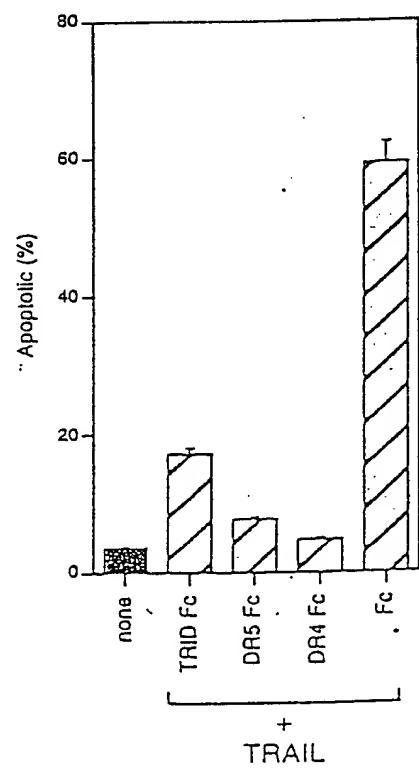


Figure 6

A



B



C

